

SUPPLEMENTAL DATA

FIGURE LEGENDS TO SUPPLEMENTARY DATA

Figure S1. Wsc1p variants are misfolded. (A) Schematic representation of HA-tagged Wsc1p and its variants. The indicated mutations are marked by asterisks. S.S., signal sequence; TM, transmembrane domain; Cyt, cytoplasmic domain. (B) Pulse-chase analysis was performed in wild type and *sec12-4* strains expressing Wsc1p and $\Delta 68-80$ as described in Figure 1B. (C) The folding status of Wsc1p and its variants were examined by a PEGylation-based folding assay as described in Figure 1D.

Figure S2. Degradation of Wsc1p variants is ERAD independent. (A-E) The turnover rates of Wsc1p variants in WT, $\Delta cue1$, $\Delta hrd1$ and $\Delta doa10$ cells were examined by pulse-chase analysis as described in Figure 2A.

Figure S3. Wsc1- $\Delta 68-80$ is stable when retained in the ER. Stability of Wsc1- $\Delta 68-80$ was examined in wild type and *sec12-4* strains using pulse-chase analysis as described in Figure 3A.

Figure S4. Wsc1p variants degrade in the vacuole. (A-B) Pulse-chase analysis was performed to examine the degradation of Wsc1p variants in wild type and $\Delta pep4$ cells as described in Figure 2A.

Figure S5. Visualization of the vacuolar ATPase by indirect immunofluorescence. Wild type cells were processed as described in Figure 3D and stained with anti-V-ATPase (60 kDa subunit) primary antibodies followed by Alexa Fluor 546 goat anti-mouse secondary antibodies. The cells

were visualized by confocal and DIC microscopy. Note that V-ATPase staining coincides with structures that appear as optical depressions using DIC. Scale bar, 5 μ m.

Figure S6. Degradation of Wsc1-L63R is autophagy independent. (A) Wild type and Δ *apg8* cells expressing Wsc1-L63R were analyzed by pulse-chase analysis as described in Figure 2A. (B) Wsc1-L63R turnover was analyzed by pulse-chase analysis in wild type and Δ *vps10* cells as described in Figure 2A.

Figure S7. Wsc1- Δ 68-80 does not contain an ERAD determinant in the luminal domain. (A) A schematic diagram of Wsc1- Δ 68-80 and Wsc1- Δ 68-80_{Luminal}. S.S., signal sequence; TM, transmembrane domain; Cyt, cytoplasmic domain. (B) The localization of Wsc1- Δ 68-80_{Luminal} was examined by indirect immunofluorescence as described in Figure 5B. Scale bar, 5 μ m. (C) The turnover of Wsc1- Δ 68-80 and Wsc1- Δ 68-80_{Luminal} in the wild type strain was measured by pulse-chase analysis as described in Figure 2A. (D) Pulse-chase analysis was performed in wild type and *sec12-4* strains expressing Wsc1- Δ 68-80_{Luminal} as described in Figure 1B.

Figure S8. Wsc1- Δ 68-80 fused with an ERAD determinant is recognized by ERAD. (A) Schematic representation of ED-Wsc1- Δ 68-80 and ED-Wsc1- Δ 68-80_{Luminal}. The CPY C-terminal domain contains a single carbohydrate and is represented by a branched symbol. S.S., signal sequence of Kar2p; CPY CTD, the CPY C-terminal domain; TM, transmembrane domain; Cyt, cytoplasmic domain. (B) The turnover of ED-Wsc1- Δ 68-80 was examined in wild type and various mutants using pulse-chase analysis as described in Figure 2A. (C) Wild type and mutant

cells expressing ED-Wsc1- Δ 68-80_{Luminal} were analyzed by pulse-chase analysis as described in Figure 2A.

SUPPLEMENTARY TABLES

Table S1. Strains used in this study

Strain	Genotype	Source
W303	<i>Mata</i> , <i>leu2-3, 112, his3-11, trp1-1, ura3-1, can1-100, ade2-1</i>	P. Walter (UCSF)
BY4742	<i>Mataα</i> , <i>leu2Δ0, lys2Δ0, his3Δ1, ura3Δ0</i>	Research Genetics, Huntsville, AL
ESY258	<i>Mata</i> , pDN436, W303 background	Spear and Ng, 2003
SWY300	<i>Mata</i> , pRS315, W303 background	This study
SWY330	<i>Mata</i> , pSW100, W303 background	This study
SWY382	<i>Mata</i> , <i>sec12-4</i> , pSW100, W303 background	This study
SWY338	<i>Mata</i> , pSW102, W303 background	This study
SWY383	<i>Mata</i> , <i>sec12-4</i> , pSW102, W303 background	This study
SWY339	<i>Mata</i> , <i>cue1::TRP1</i> , pSW102, W303 background	This study
SWY340	<i>Mata</i> , <i>hrd1::KANMX</i> , pSW102, W303 background	This study
SWY614	<i>Mata</i> , <i>doa10::KANMX</i> , pSW102, W303 background	This study
SWY341	<i>Mata</i> , <i>pep4::HIS3</i> , pSW102, W303 background	This study
SWY342	<i>Mata</i> , pSW104, W303 background	This study
SWY384	<i>Mata</i> , <i>sec12-4</i> , pSW104, W303 background	This study
SWY343	<i>Mata</i> , <i>cue1::TRP1</i> , pSW104, W303 background	This study
SWY344	<i>Mata</i> , <i>hrd1::KANMX</i> , pSW104, W303 background	This study
SWY367	<i>Mata</i> , <i>doa10::KANMX</i> , pSW104, W303 background	This study
SWY345	<i>Mata</i> , <i>pep4::HIS3</i> , pSW104, W303 background	This study
SWY416	<i>Mata</i> , <i>vps10::KANMX</i> , pSW104, W303 background	This study
SWY653	<i>Mata</i> , <i>ktr1::KANMX, ktr3::KANMX, kre2::TRP1</i> , pSW104, W303 background	This study
SWY402	<i>Mataα</i> , pSW104, BY4742 background	This study
SWY403	<i>Mataα</i> , <i>apg8::KANMX</i> , pSW104, BY4742 background	This study
SWY346	<i>Mata</i> , pSW105, W303 background	This study
SWY385	<i>Mata</i> , <i>sec12-4</i> , pSW105, W303 background	This study
SWY347	<i>Mata</i> , <i>cue1::TRP1</i> , pSW105, W303 background	This study
SWY348	<i>Mata</i> , <i>hrd1::KANMX</i> , pSW105, W303 background	This study
SWY615	<i>Mata</i> , <i>doa10::KANMX</i> , pSW105, W303 background	This study
SWY349	<i>Mata</i> , <i>pep4::HIS3</i> , pSW105, W303 background	This study
SWY354	<i>Mata</i> , pSW112, W303 background	This study
SWY387	<i>Mata</i> , <i>sec12-4</i> , pSW112, W303 background	This study
SWY355	<i>Mata</i> , <i>cue1::TRP1</i> , pSW112, W303 background	This study
SWY356	<i>Mata</i> , <i>hrd1::KANMX</i> , pSW112, W303 background	This study
SWY369	<i>Mata</i> , <i>doa10::KANMX</i> , pSW112, W303 background	This study

SWY357	<i>Mata, pep4::HIS3</i> , pSW112, W303 background	This study
SWY358	<i>Mata</i> , pSW113, W303 background	This study
SWY388	<i>Mata, sec12-4</i> , pSW113, W303 background	This study
SWY359	<i>Mata, cue1::TRP1</i> , pSW113, W303 background	This study
SWY360	<i>Mata, hrd1::KANMX</i> , pSW113, W303 background	This study
SWY371	<i>Mata, doa10::KANMX</i> , pSW113, W303 background	This study
SWY361	<i>Mata, pep4::HIS3</i> , pSW113, W303 background	This study
SWY420	<i>Mata, vps10::KANMX</i> , pSW113, W303 background	This study
SWY362	<i>Mata</i> , pSW114, W303 background	This study
SWY389	<i>Mata, sec12-4</i> , pSW114, W303 background	This study
SWY363	<i>Mata, cue1::TRP1</i> , pSW114, W303 background	This study
SWY364	<i>Mata, hrd1::KANMX</i> , pSW114, W303 background	This study
SWY376	<i>Mata, doa10::KANMX</i> , pSW114, W303 background	This study
SWY365	<i>Mata, pep4::HIS3</i> , pSW114, W303 background	This study
SWY423	<i>Mata</i> , pSW119, W303 background	This study
SWY508	<i>Mata, sec12-4</i> , pSW119, W303 background	This study
SWY458	<i>Mata</i> , pSW122, W303 background	This study
SWY511	<i>Mata, sec12-4</i> , pSW122, W303 background	This study
SWY541	<i>Mata</i> , pSW144, W303 background	This study
SWY543	<i>Mata, cue1::TRP1</i> , pSW144, W303 background	This study
SWY544	<i>Mata, hrd1::KANMX</i> , pSW144, W303 background	This study
SWY542	<i>Mata, pep4::HIS3</i> , pSW144, W303 background	This study
SWY561	<i>Mata, pep4::HIS3, cue1::TRP1</i> , pSW144, W303 background	This study
SWY562	<i>Mata, pep4::HIS3, hrd1::KANMX</i> , pSW144, W303 background	This study
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SWY547	<i>Mata, cue1::TRP1</i> , pSW145, W303 background	This study
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SWY546	<i>Mata, pep4::HIS3</i> , pSW145, W303 background	This study
SWY564	<i>Mata, pep4::HIS3, cue1::TRP1</i> , pSW145, W303 background	This study
SWY565	<i>Mata, pep4::HIS3, hrd1::KANMX</i> , pSW145, W303 background	This study
SWY579	<i>Mata</i> , pSW153, W303 background	This study
SWY581	<i>Mata, cue1::TRP1</i> , pSW153, W303 background	This study
SWY582	<i>Mata, hrd1::KANMX</i> , pSW153, W303 background	This study
SWY580	<i>Mata, pep4::HIS3</i> , pSW153, W303 background	This study
SWY587	<i>Mata</i> , pSW155, W303 background	This study
SWY589	<i>Mata, cue1::TRP1</i> , pSW155, W303 background	This study
SWY590	<i>Mata, hrd1::KANMX</i> , pSW155, W303 background	This study
SWY588	<i>Mata, pep4::HIS3</i> , pSW155, W303 background	This study
SWY601	<i>Mata</i> , pSW156, W303 background	This study
SWY603	<i>Mata</i> , pSW157, W303 background	This study
SWY604	<i>Mata, pep4::HIS3</i> , pSW157, W303 background	This study
SWY605	<i>Mata</i> , pSW158, W303 background	This study
SWY606	<i>Mata, pep4::HIS3</i> , pSW158, W303 background	This study

Table S2. Plasmids modified by site-directed mutagenesis

Plasmid	Protein	Primer	Mutation	Template	Vector	Source
pSW102	Wsc1-L31R	SWN64	L31R	pSW100	pRS315	This study
pSW104	Wsc1-L63R	SWN66	L63R	pSW100	pRS315	This study
pSW105	Wsc1-C98R/ G99R	SWN67	C98R, G99R	pSW100	pRS315	This study
pSW112	Wsc1-Δ34-44	SWN72	Deletion of D34 to Q44	pSW100	pRS315	This study
pSW113	Wsc1-Δ68-80	SWN73	Deletion of E68 to E80	pSW100	pRS315	This study
pSW114	Wsc1-Δ96-110	SWN74	Deletion of to E96 to D110	pSW100	pRS315	This study
pSW119	Wsc1-L63R Luminal	SWN76	Deletion of DNA TMD and Cytoplasmic domains of Wsc1- L63R (Deletion of V262 to D378) Deletion of DNA TMD and	pSW104	pRS315	This study
pSW122	Wsc1-Δ68-80 Luminal	SWN76	cytoplasmic domains of Wsc1 Δ68-80 Deletion of DNA TMD and	pSW113	pRS315	This study
pSW153	ED-Wsc1- L63R _{Luminal}	SWN76	cytoplasmic domains of ED- Wsc1-L63R Deletion of DNA TMD and	pSW144	pRS315	This study
pSW155	ED-Wsc1-Δ68- 80 _{Luminal}	SWN76	cytoplasmic domains of ED- Wsc1-Δ68-80	pSW145	pRS315	This study
pSW156	Wsc1-AAA	SWN77	N344A, P345A, F346A	pSW147	pRS315	This study
pSW157	Wsc1-L63R- AAA	SWN77	N344A, P345A, F346A	pSW148	pRS315	This study
pSW158	Wsc1-Δ68-80- AAA	SWN77	N331A, P332A, F333A	pSW149	pRS315	This study

Table S3. Oligonucleotide primers used in this study

Primer	Construct	Sequence (5'→3')
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SWN1	pSW3	CGCGGATCCATGAGACCGAACAAAAACAAGTC
SWN2	pSW3	CTCATGCCATGGCATCAGCTTCGTCTGGATTGACC
SWN50	pSW144, pSW145	GTTTCCCGACTGGAAAAGCGGGCAGTG
SWN64	pSW102	GAATACGTGAATTGTTTTAGCTCAAGACCCTCTGACTTTTTCAAAGGCCGA
SWN66	pSW104	CGCAAAAGGTGCAAGCTACTTTGCCAGATATAATCATTGAGAAATGTTATTGTG
SWN67	pSW105	CTTTGGTTACAGCAGTGAGATGTGTAGAAGAGAAGATGCCTATTCTGTGTACCAAC
SWN72	pSW112	GAATTGTTTTAGCTCACTACCCTCTTCGAGTTCACACTGTAACAGTGAG
SWN73	pSW113	CTACTTTGCCCTTTATAATCATTTCATCTACTTCTCTTCATGTAATACG
SWN74	pSW114	ATACGTATTGCTTTGGTTACAGCAGTTCTGACACAAATAGCAATAGCATAAG
	pSW119,	
SWN76	pSW122, pSW153, pSW155	GTAAAACTCATAAAAAGAAAGCCAATGCCATGGCCTACCCATATGATGTTC
	pSW156,	
SWN77	pSW157, pSW158	GCACACCAAAGGGCAAACCTGATATTGCCGCCGCCGACACTCAAGGAGAATAAGTA ACG
	pSW144,	
SWN84	pSW145	GGAAAAAAGCGGCCCAATTCCGTATATGATGATACATATGTTAGGTC
	pSW144,	
SWN85	pSW145	TAAGGAGAAACCACCGTGGATCCATTCG
	pSW144,	
SWN86	pSW145	TATGAATACGTGAATTGTTTTAGCTCACTACC
	pSW147,	
SWN87	pSW148, pSW149	ATAAGAATGCGGCCGCGGAAGGCACCCTTTTCGAAGG
	pSW147,	
SWN88	pSW148, pSW149	ACATGGATCCTGTTGAGATTTAGCTGTGTTTGTG

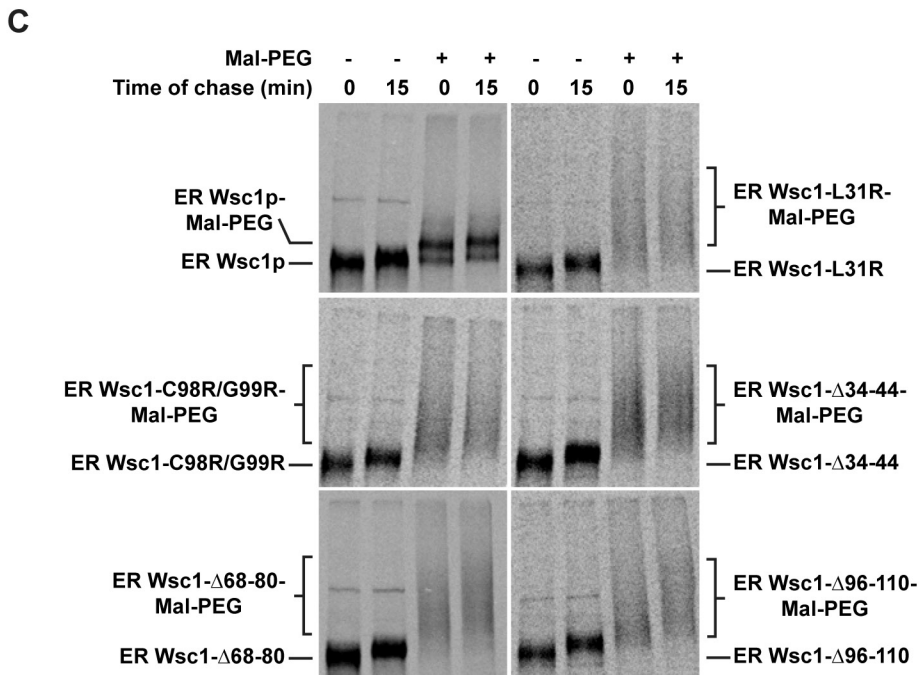
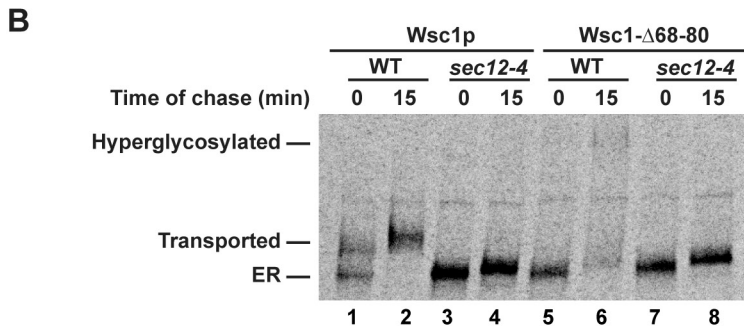
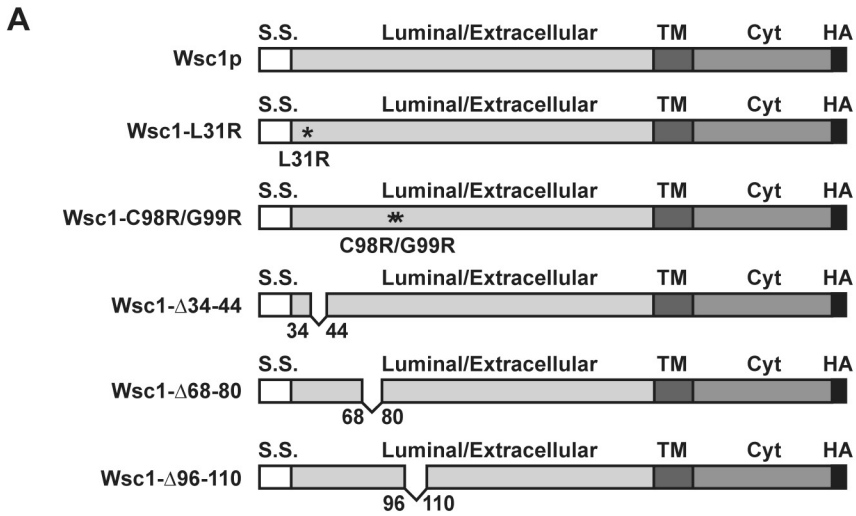


Figure S1

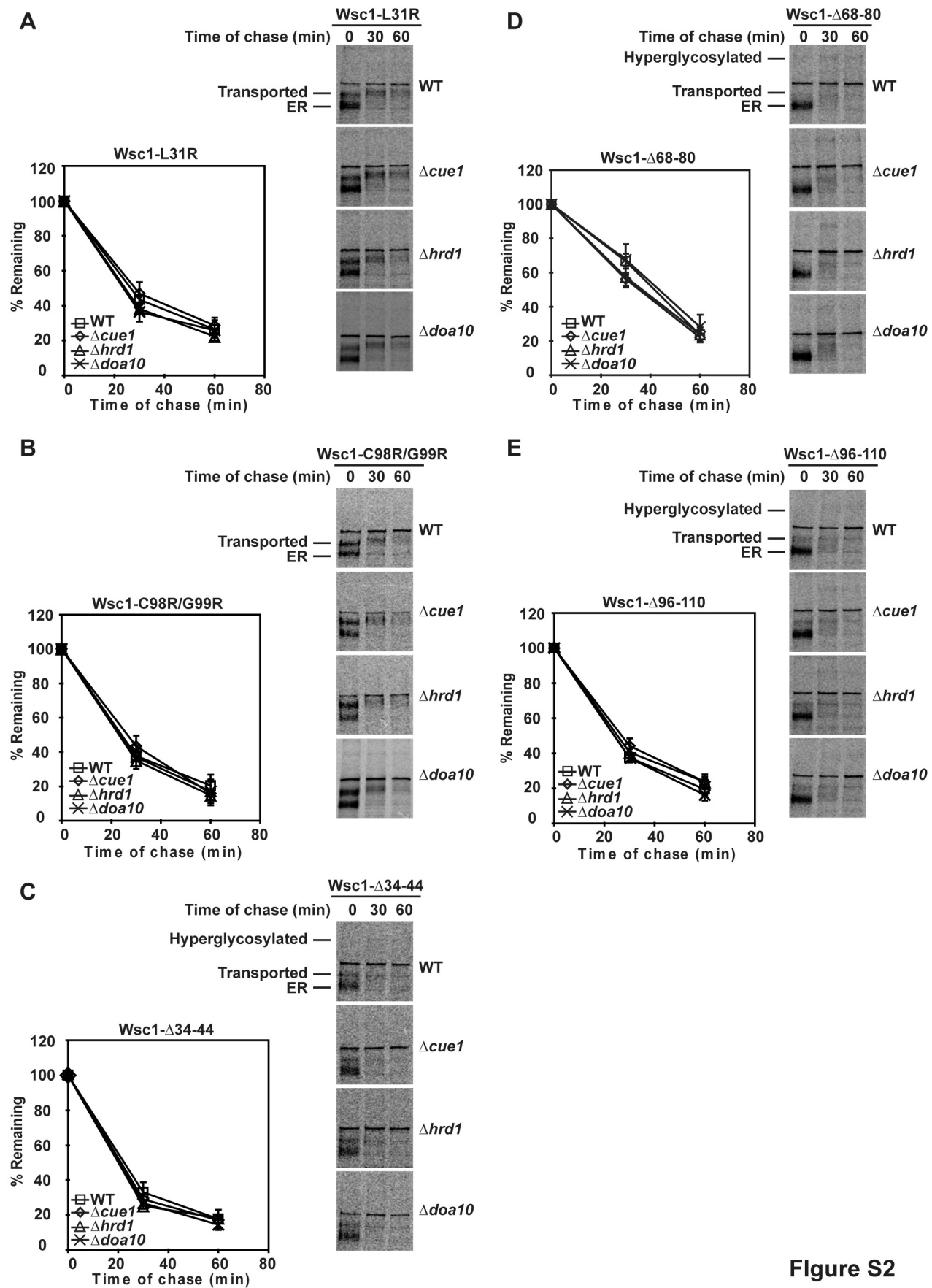


Figure S2

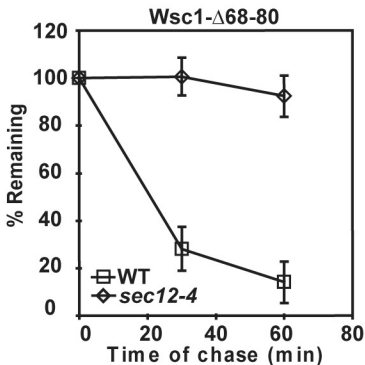
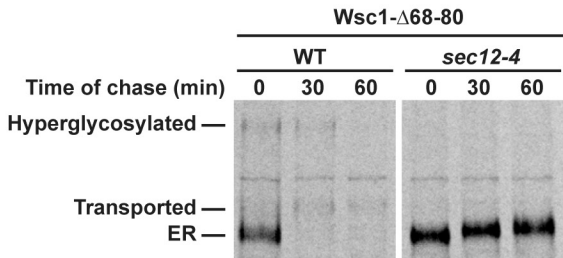
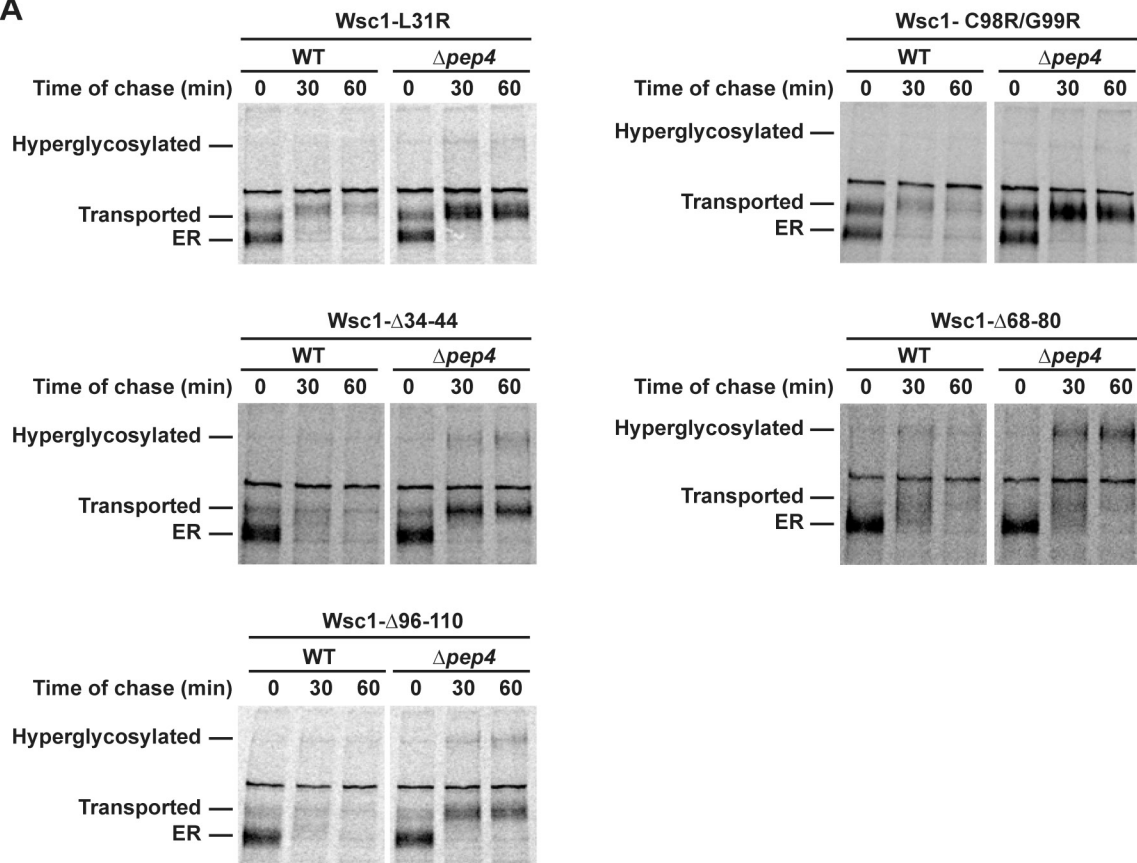
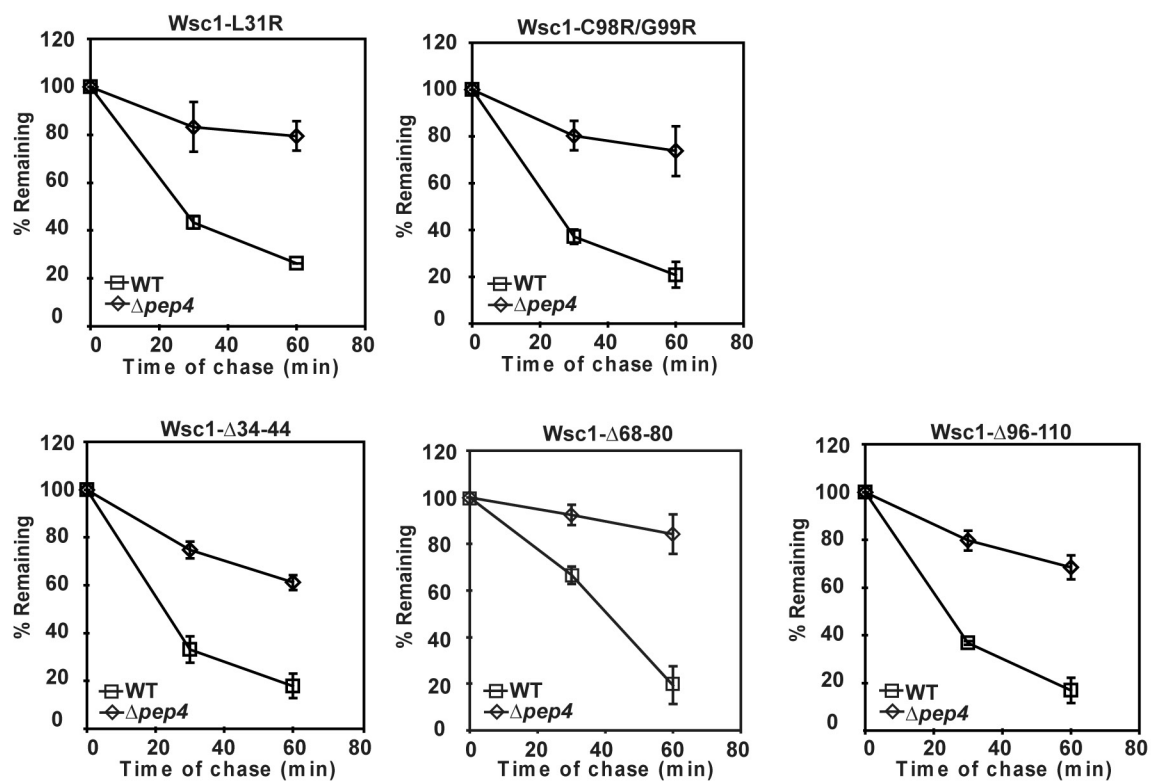


Figure S3

A**B****Figure S4**

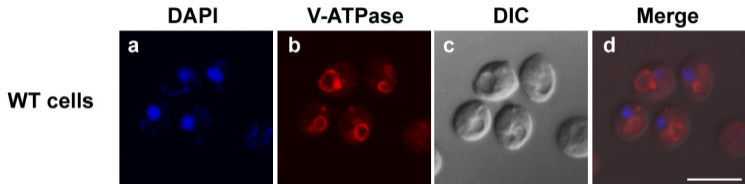
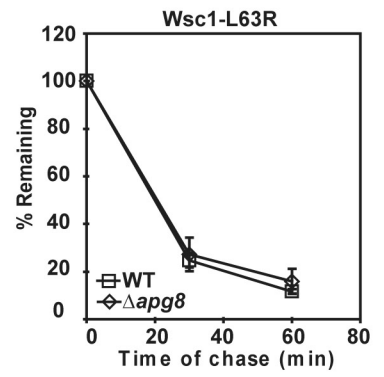
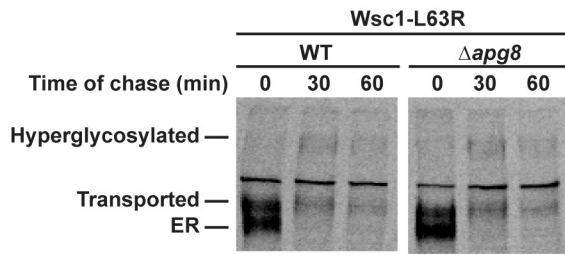
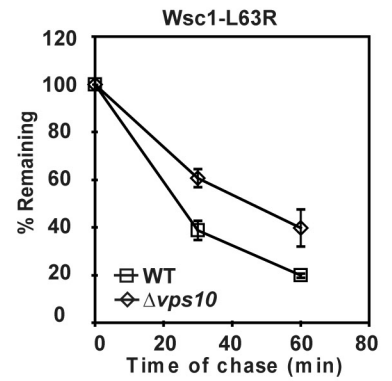
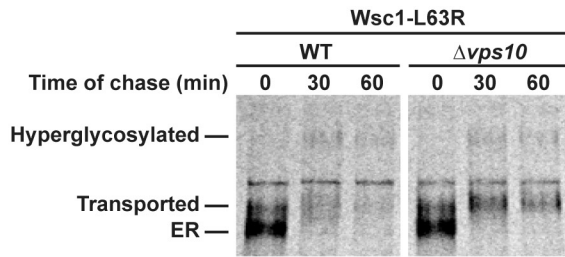


Figure S5

A**B**

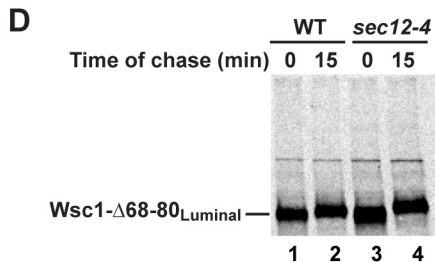
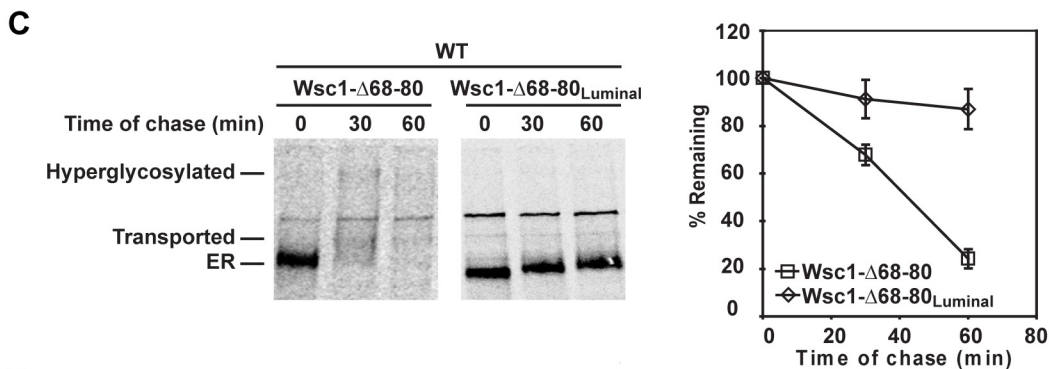
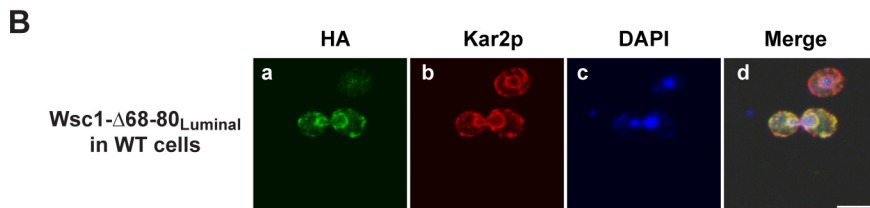
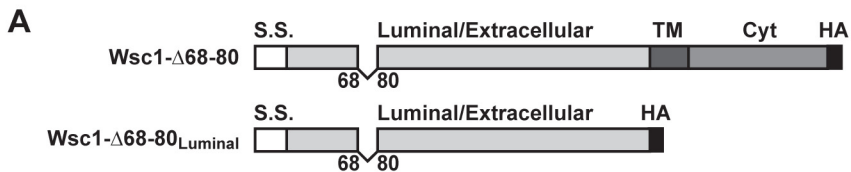


Figure S7

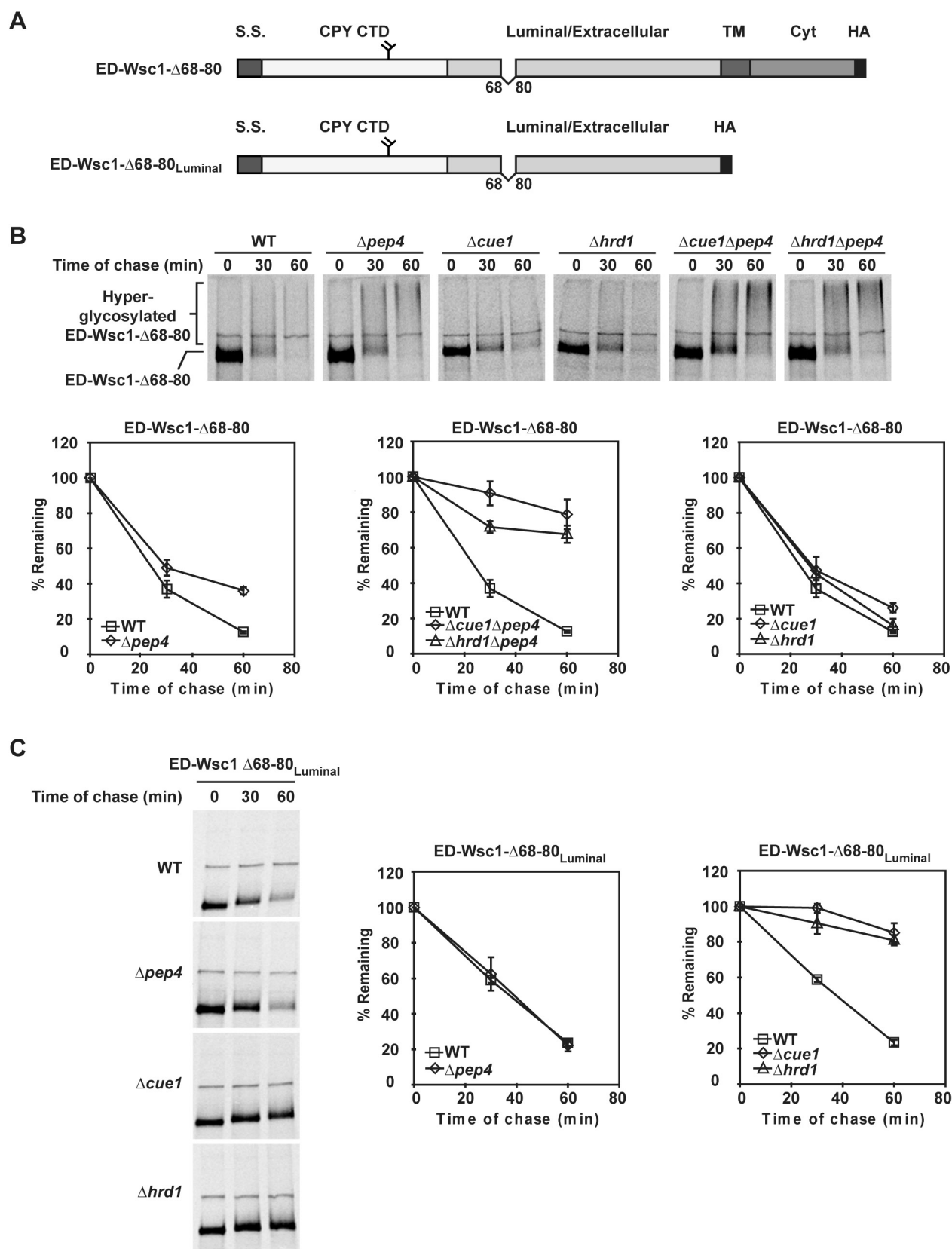


Figure S8